

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/530,217

Source: PCT

Date Processed by STIC: 4-12-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/12/2005

PATENT APPLICATION: US/10/530,217

TIME: 14:05:35

Input Set : A:\082368-003910US.txt

Output Set: N:\CRF4\04122005\J530217.raw

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4 <110> APPLICANT: Nakamura, Yusuke
5     Katagiri, Toyomasa
7 <120> TITLE OF INVENTION: GENES AND POLYPEPTIDES RELATING TO HUMAN
8     MYELOID LEUKEMIA
10 <130> FILE REFERENCE: 082368-003910US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/530,217
C--> 12 <141> CURRENT FILING DATE: 2005-03-30
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/09589
13 <151> PRIOR FILING DATE: 2003-07-29
15 <150> PRIOR APPLICATION NUMBER: US 60/414,867
16 <151> PRIOR FILING DATE: 2002-09-30
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 22
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
29     RT-PCR
31 <400> SEQUENCE: 1
32 gtgctcttcc tcttcacctt tg                                22
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 23
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
41     RT-PCR
44 <400> SEQUENCE: 2
45 ggtggtcgtc aagaaacaag tta                                23
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 23
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
54     RT-PCR
56 <400> SEQUENCE: 3
57 catccacgaa actaccttca act                                23
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 23
61 <212> TYPE: DNA

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62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
66     RT-PCR
68 <400> SEQUENCE: 4
69 tctccttaga gagaagtggg gtg                23
71 <210> SEQ ID NO: 5
72 <211> LENGTH: 22
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
78     RT-PCR
80 <400> SEQUENCE: 5
81 gtgctcttcc tcttcacctt tg                22
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 23
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
89 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
90     RT-PCR
92 <400> SEQUENCE: 6
93 ggtggtcgtc aagaaacaag tta                23
95 <210> SEQ ID NO: 7
96 <211> LENGTH: 23
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
100 <220> FEATURE:
101 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
102     RT-PCR
104 <400> SEQUENCE: 7
105 gacaactcac tcaagattgt cag                23
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 20
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
115     RT-PCR
117 <400> SEQUENCE: 8
118 gatccacgac ggacacattg                20
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 28
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
127     RT-PCR

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129 <400> SEQUENCE: 9
130 cggaattccg atgagtgagg cccgcagg                28
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 29
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
139     RT-PCR
141 <400> SEQUENCE: 10
142 ggggtacccc agtggagctg agcgtccag                29
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 18
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Artificially synthesized S-oligonucleotide
151     sequence for antisense
153 <400> SEQUENCE: 11
154 ctgtgtgatg gacgtctg                            18
156 <210> SEQ ID NO: 12
157 <211> LENGTH: 18
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: S-oligonucleotide sequence for antisense
164 <400> SEQUENCE: 12
165 gtctgcagggt agtgtgtc                            18
167 <210> SEQ ID NO: 13
168 <211> LENGTH: 19
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Target sequence for siRNA
175 <400> SEQUENCE: 13
176 gtacgtgcag caggagaac                            19
178 <210> SEQ ID NO: 14
179 <211> LENGTH: 19
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Target sequence for siRNA
186 <400> SEQUENCE: 14
187 gaagcagcac gacttcttc                            19
189 <210> SEQ ID NO: 15
190 <211> LENGTH: 2958
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
194 <220> FEATURE:

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195 <221> NAME/KEY: CDS
196 <222> LOCATION: (111)...(2678)
198 <400> SEQUENCE: 15
199 ctcggcgcgcg gcgcccctccc ggccagcgccg gccagcccct cctccccggc gccctcagga 60
200 cccccagag acccccggcg gcggcagcct gccttgctct gccaggaacc atg agt 116
201 Met Ser
202 1
204 gag gcc cgc agg gac agc acg agc agc ctg cag cgc aag aag cca ccc 164
205 Glu Ala Arg Arg Asp Ser Thr Ser Ser Leu Gln Arg Lys Lys Pro Pro
206 5 10 15
208 tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag 212
209 Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
210 20 25 30
212 ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg 260
213 Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
214 35 40 45 50
216 agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 308
217 Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
218 55 60 65
220 cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc 356
221 Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
222 70 75 80
224 agg ggg acc gcc gac tgg ttt gga gtg agc aag gac agt gac agc acc 404
225 Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp Ser Thr
226 85 90 95
228 cag aaa tgg cag cgc aag agc atc cgt cac tgc agc cag cgc tac ggg 452
229 Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg Tyr Gly
230 100 105 110
232 aag ctg aag ccc cag gtc ctc cgg gag ctg gac ctg ccc agc cag gac 500
233 Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
234 115 120 125 130
236 aac gtg tcg ctg acc agc acc gag acg cca ccc cca ctc tac gtg ggg 548
237 Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr Val Gly
238 135 140 145
240 cca tgc cag ctg ggc atg cag aag atc ata gac ccc ctg gcc cgt ggc 596
241 Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly
242 150 155 160
244 cgt gcc ttc cgt gtg gca gat gac act gcg gaa ggc ctg agt gcc cca 644
245 Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser Ala Pro
246 165 170 175
248 cac act ccc gtc acg ccg ggt gct gcc tcc ctc tgc tcc ttc tcc agc 692
249 His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe Ser Ser
250 180 185 190
252 tcc cgc tca ggt ttc cac cgg ctc ccg cgg cgg cgc aag cga gag tcg 740
253 Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg Glu Ser
254 195 200 205 210
256 gtg gcc aag atg agc ttc cgg gcg gcc gca gcg ctg atg aaa ggc cgc 788
257 Val Ala Lys Met Ser Phe Arg Ala Ala Ala Leu Met Lys Gly Arg
258 215 220 225

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260	tcc	gtt	agg	gat	ggc	acc	ttt	cgc	cgg	gca	cgg	cgt	cga	agc	ttc	act	836
261	Ser	Val	Arg	Asp	Gly	Thr	Phe	Arg	Arg	Ala	Arg	Arg	Arg	Ser	Phe	Thr	
262				230					235					240			
264	cca	gct	agc	ttt	ctg	gag	gag	gac	aca	act	gat	ttc	ccc	gat	gag	ctg	884
265	Pro	Ala	Ser	Phe	Leu	Glu	Glu	Asp	Thr	Thr	Asp	Phe	Pro	Asp	Glu	Leu	
266			245					250					255				
268	gac	aca	tcc	ttc	ttt	gcc	cgg	gaa	ggt	atc	ctc	cat	gaa	gag	ctg	tcc	932
269	Asp	Thr	Ser	Phe	Phe	Ala	Arg	Glu	Gly	Ile	Leu	His	Glu	Glu	Leu	Ser	
270		260					265					270					
272	aca	tac	ccg	gat	gaa	gtt	ttc	gag	tcc	cca	tcg	gag	gca	gcg	cta	aag	980
273	Thr	Tyr	Pro	Asp	Glu	Val	Phe	Glu	Ser	Pro	Ser	Glu	Ala	Ala	Leu	Lys	
274	275					280					285				290		
276	gac	tgg	gag	aag	gca	ccg	gag	cag	gcg	gac	ctc	acc	ggc	ggg	gcc	ctg	1028
277	Asp	Trp	Glu	Lys	Ala	Pro	Glu	Gln	Ala	Asp	Leu	Thr	Gly	Gly	Ala	Leu	
278				295					300					305			
280	gac	cgc	agc	gag	ctt	gag	cgc	agc	cac	ctg	atg	ctg	ccc	ttg	gag	cga	1076
281	Asp	Arg	Ser	Glu	Leu	Glu	Arg	Ser	His	Leu	Met	Leu	Pro	Leu	Glu	Arg	
282			310					315					320				
284	ggc	tgg	cgg	aag	cag	aag	gag	ggc	gcc	gca	gcc	ccg	cag	ccc	aag	gtg	1124
285	Gly	Trp	Arg	Lys	Gln	Lys	Glu	Gly	Ala	Ala	Ala	Pro	Gln	Pro	Lys	Val	
286			325				330					335					
288	cgg	ctc	cga	cag	gag	gtg	gtg	agc	acc	gcg	ggg	ccg	cga	cgg	ggc	cag	1172
289	Arg	Leu	Arg	Gln	Glu	Val	Val	Ser	Thr	Ala	Gly	Pro	Arg	Arg	Gly	Gln	
290		340				345					350						
292	cgt	atc	gcg	gtg	ccg	gtg	cgc	aag	ctc	ttc	gcc	cgg	gag	aag	cgg	ccg	1220
293	Arg	Ile	Ala	Val	Pro	Val	Arg	Lys	Leu	Phe	Ala	Arg	Glu	Lys	Arg	Pro	
294	355				360				365				370				
296	tat	ggg	ctg	ggc	atg	gtg	gga	cgg	ctc	acc	aac	cgc	acc	tac	cgc	aag	1268
297	Tyr	Gly	Leu	Gly	Met	Val	Gly	Arg	Leu	Thr	Asn	Arg	Thr	Tyr	Arg	Lys	
298				375				380					385				
300	cgc	atc	gac	agc	ttc	gtc	aag	cgc	cag	atc	gag	gac	atg	gac	gac	cac	1316
301	Arg	Ile	Asp	Ser	Phe	Val	Lys	Arg	Gln	Ile	Glu	Asp	Met	Asp	Asp	His	
302			390					395					400				
304	agg	ccc	ttc	ttc	acc	tac	tgg	ctt	acc	ttc	gtg	cac	tcg	ctc	gtc	acc	1364
305	Arg	Pro	Phe	Phe	Thr	Tyr	Trp	Leu	Thr	Phe	Val	His	Ser	Leu	Val	Thr	
306			405				410					415					
308	atc	cta	gcc	gtg	tgc	atc	tat	ggc	atc	gcg	ccc	gtg	ggc	ttc	tcg	cag	1412
309	Ile	Leu	Ala	Val	Cys	Ile	Tyr	Gly	Ile	Ala	Pro	Val	Gly	Phe	Ser	Gln	
310		420				425					430						
312	cat	gag	acg	gtg	gac	tcg	gtg	ctg	cgg	aac	cgc	ggg	gtc	tac	gag	aac	1460
313	His	Glu	Thr	Val	Asp	Ser	Val	Leu	Arg	Asn	Arg	Gly	Val	Tyr	Glu	Asn	
314	435				440				445				450				
316	gtc	aag	tac	gtg	cag	cag	gag	aac	ttc	tgg	atc	ggg	ccc	agc	tcg	gag	1508
317	Val	Lys	Tyr	Val	Gln	Gln	Glu	Asn	Phe	Trp	Ile	Gly	Pro	Ser	Ser	Glu	
318			455				460					465					
320	gcc	ctc	atc	cac	ctg	ggc	gcc	aag	ttt	tcg	ccc	tgc	atg	cgc	cag	gac	1556
321	Ala	Leu	Ile	His	Leu	Gly	Ala	Lys	Phe	Ser	Pro	Cys	Met	Arg	Gln	Asp	
322			470				475					480					
324	ccg	cag	gtg	cac	agc	ttc	att	cgc	tcg	gcg	cgc	gag	cgc	gag	aag	cac	1604

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date